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AMENDMENTS TO THE CLAIMS;

This listing of claims will replace all prior versions and listing of the claims in the application:

LISTING OF THE CLAIMS:

Claim 1. (Currently amended) A method for preparing a variant polynucleotide having a different nucleotide sequence from at least two parent polynucleotides comprising;

preparing at least one heteroduplex between said at least ~~said~~ two parent polynucleotides,

cleaving at least one polynucleotide strand in said heteroduplex at a mismatch site with an effective amount of mismatch-directed strand cleavage activity to form a cleavage site,

replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site,

wherein at least one of said polynucleotide strands has a different nucleotide sequence from either of said at least two parent polynucleotides.

Claim 2. (Original) The method of claim 1 wherein the polynucleotides forming a heteroduplex are circular.

Claim 3. (Cancelled)

Claim 4. (Currently amended) The method of claim 1 wherein ~~the~~ said at least one heteroduplex ~~polynucleotide sequence~~ contains a gene.

Claim 5. (Currently amended) The method of claim 4 wherein ~~the~~ said at least one heteroduplex ~~polynucleotide sequence~~ is a genome.

Claim 6. (Original) The method of claim 4 wherein the heteroduplex polynucleotide sequence is a region within a polynucleotide molecule of greater than about 100bp.

Claim 7. (Currently amended) ~~The method of claim 1 wherein at least three parental polynucleotides are used.~~ A method for preparing a variant polynucleotide having a different nucleotide sequence from at least three parent polynucleotides comprising;

preparing at least two different heteroduplexes among said at least three parent polynucleotides,

cleaving at least one polynucleotide strand in said heteroduplexes at a mismatch site with an effective amount of mismatch-directed strand cleavage activity to form a cleavage site,

replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site,

wherein at least one of said polynucleotide strands has a different nucleotide sequence from any of said at least three parent polynucleotides.

Claim 8. (original) The method of claim 1 wherein a plurality of variant polynucleotides are formed.

Claim 9. (Previously presented) A method for obtaining a polynucleotide sequence encoding a desired functional property comprising;

preparing at least one heteroduplex from at least two parent polynucleotides;

cleaving at least one polynucleotide strand in said heteroduplex at a mismatch site with an effective amount of mismatch-directed strand cleavage activity to form a cleavage site,

replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site, wherein a plurality of variant polynucleotide strands are formed which have different nucleotide sequences from either of said at least two parent polynucleotides forming a population of variants, and

screening or selecting ~~a~~ said population of variants for the desired functional property.

Claim 10. (Previously presented) The method of claim 9 further comprising;

forming a second heteroduplex containing at least one variant polynucleotide strand,

cleaving at least one polynucleotide strand in said second heteroduplex at a mismatch site to form a cleavage site,

replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site, wherein a plurality of variant polynucleotide strands are formed which have different nucleotide sequences from either parent polynucleotides present in said second heteroduplex forming a population of variants, and

screening or selecting ~~a~~ said population of variants for the desired functional property.

Claim 11. (Original) The method of claim 9 further comprising converting said variant polynucleotide to RNA before said screening or selecting.

Claim 12. (Original) The method of claim 9 further comprising translating said variant polynucleotide or an RNA transcribed therefrom to produce a polypeptide and wherein said screening or selecting is performed on said polypeptide.

Claims 13-41 (Canceled)

Claim 42. (Previously presented) An *in vitro* method of making a population of sequence variants from a heteroduplex polynucleotide sequence wherein said heteroduplex polynucleotide sequence has at least two non-complementary nucleotide base pairs comprising;

mixing copies of the heteroduplex polynucleotide sequence with an effective amount of mismatch-directed strand cleavage activity, proofreading activity, and ligase activity; and allowing sufficient time for a number of non-complementary nucleotide base pairs to be converted to complementary base pairs, wherein a diverse population of polynucleotide sequences results.

Claim 43. (Previously presented) An *in vitro* method of obtaining a polynucleotide sequence encoding a desired functional property comprising;

preparing at least one heteroduplex polynucleotide sequence;

mixing copies of the heteroduplex polynucleotide sequence with an effective amount of mismatch-directed strand cleavage activity, proofreading activity, and ligase activity;

allowing sufficient time for the percentage of complementarity between strands of the heteroduplex polynucleotide sequence to increase, wherein a diverse population of polynucleotide sequences results, and

screening or selecting said population of variants for said desired functional property.